

Analysis of 17724 (399 aa)

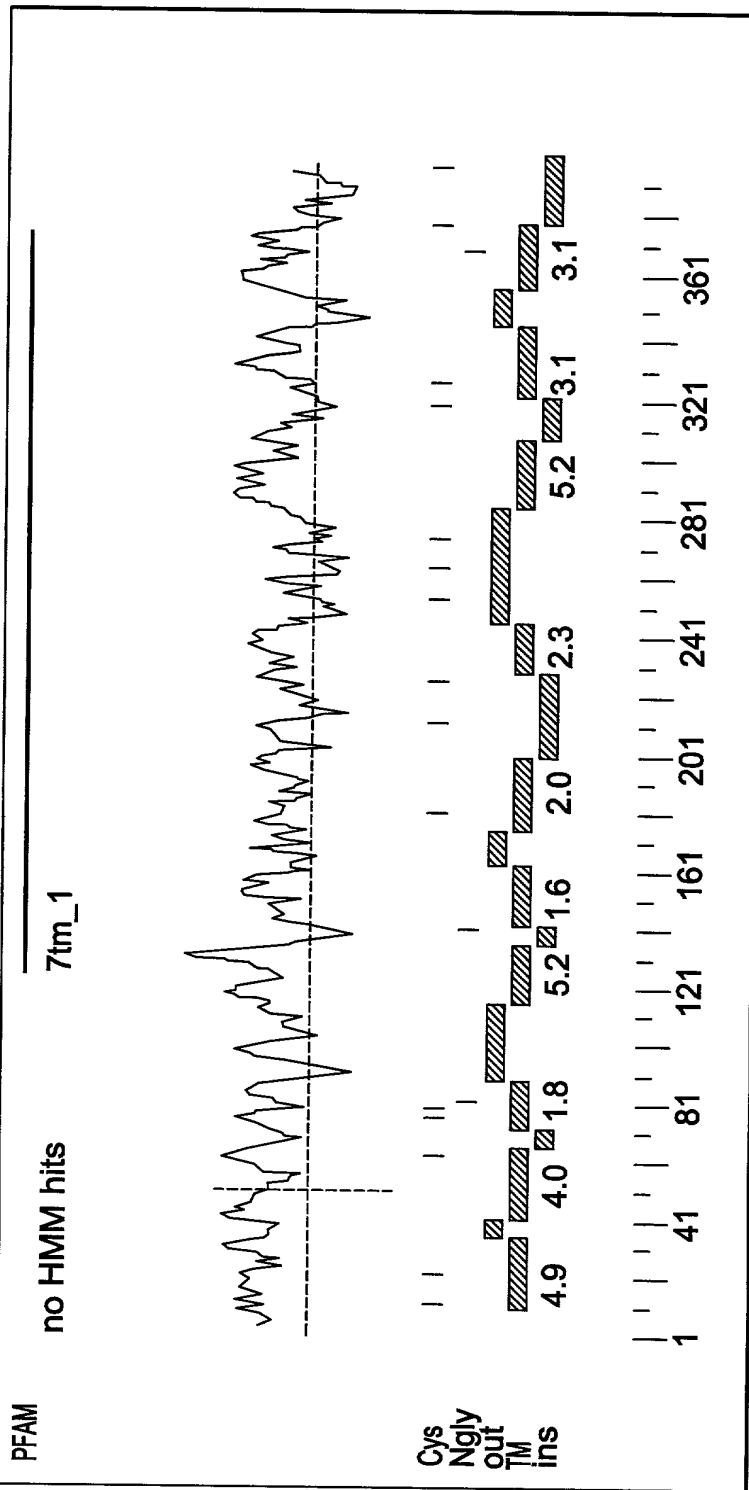
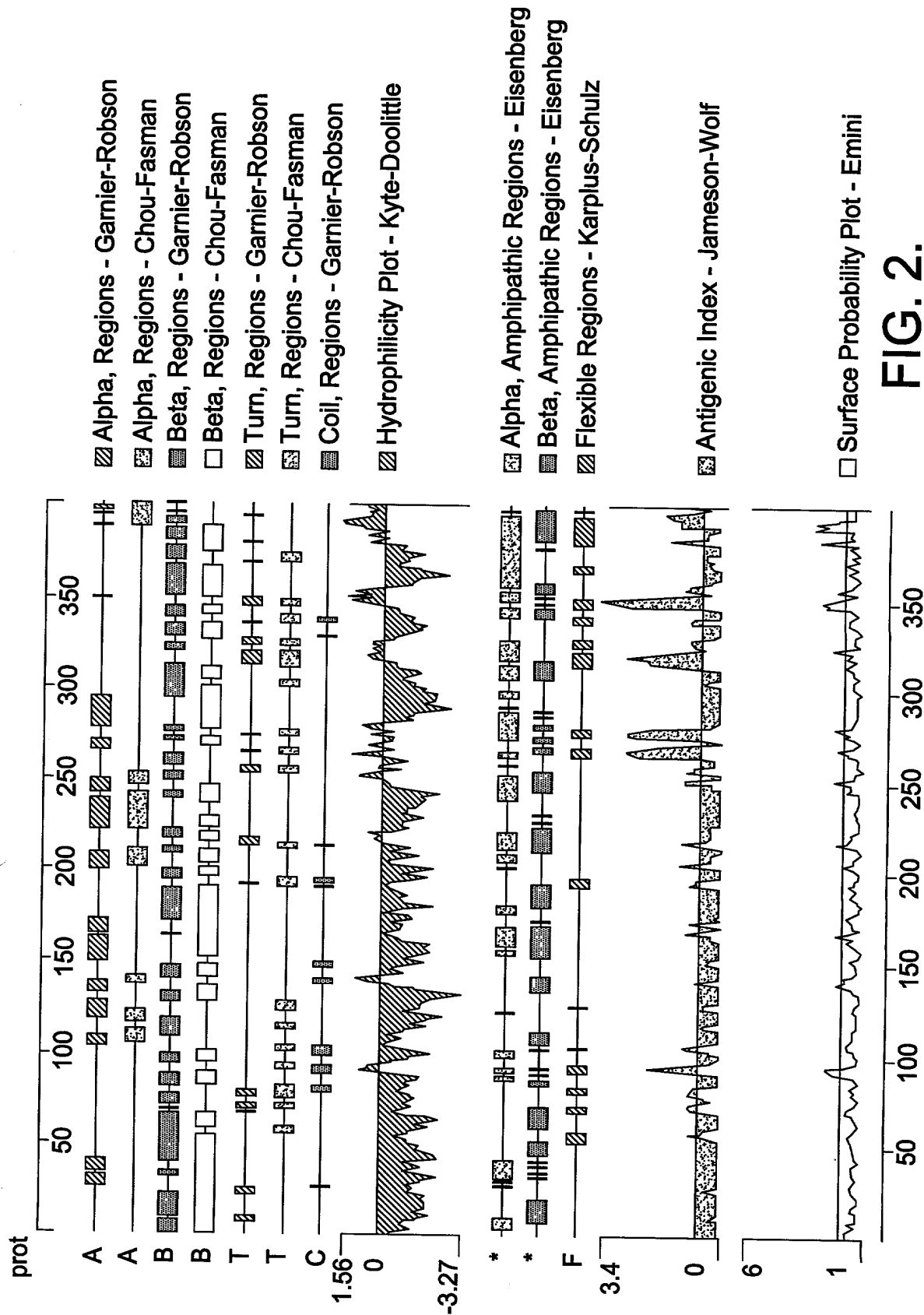


FIG. 1.



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Query: 17724

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
7tm_1	7 transmembrane receptor (rhodopsin family)	94.1	6.1e-29	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
7tm_1	1/1	125	374	..	1 259 ()	94.1	6.1e-29

Alignments of top-scoring domains:

7tm_1: domain 1 of 1, from 125 to 374: score 94.1, E = 6.1e-29

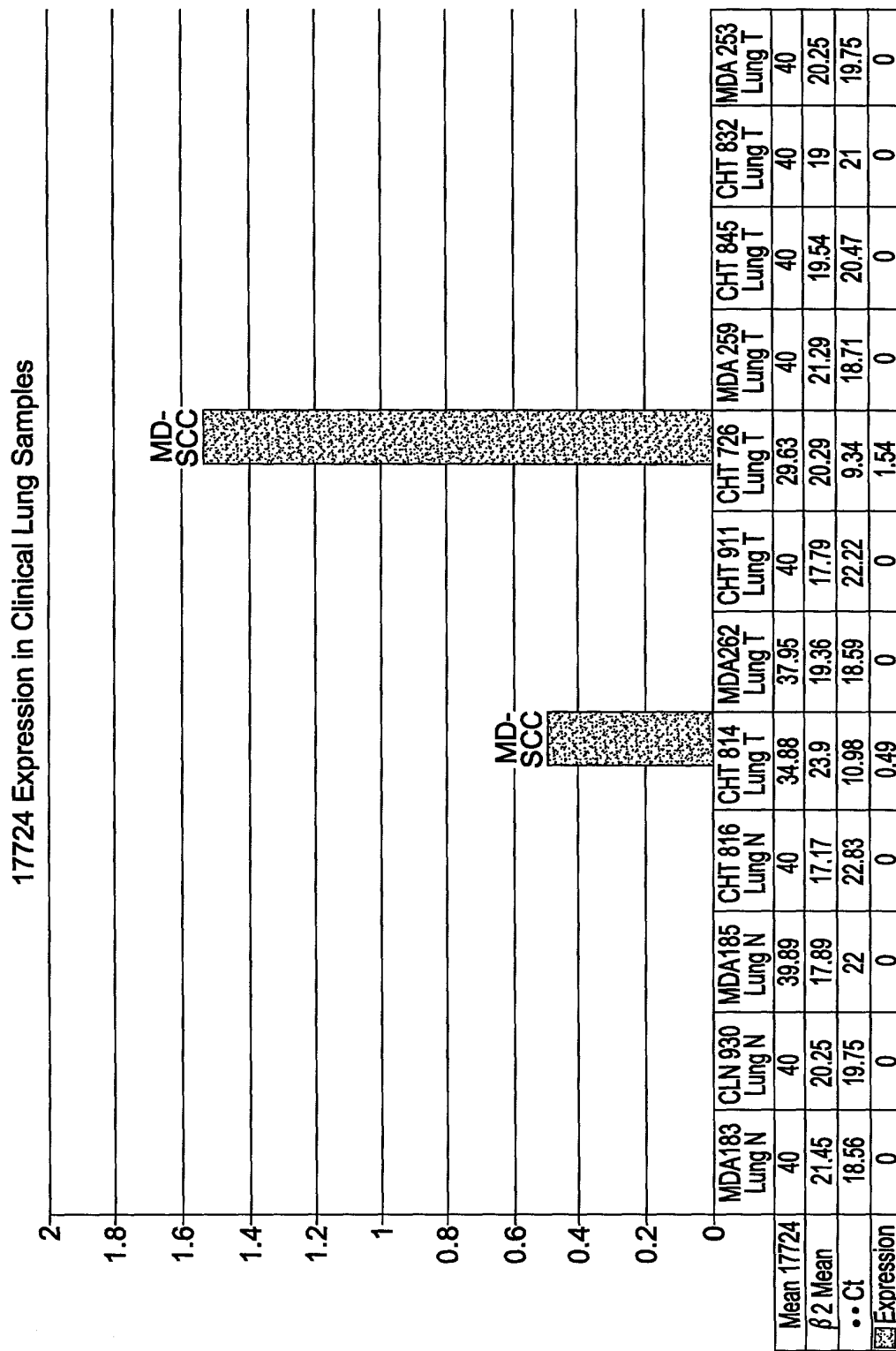
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*->GNILVilvrlrttklrtpnifiINLAvADLLflltppwalyylvg
    GN ++i+ ++ +l+tp+++f++N ++ +L++ t +p +l+ l+
17724 125 GNTIIIVMVIADTHLHTPMYFFLGNSLLEILVTMTAVPRMLS DLLV 171
    gsedWpfGsaICklvtaldvvnmyaSi l l l taISiDRYIAIvhPlryrrr
    ++++ +C ++ ++ + + +S l Lt +++DR++AI+hPlry ++
17724 172 --PHKVITFTGCMVQFYHFSLGSTSFLILTDMALDRFVAICHPLRYGTL 219
    rtsprrrAkvvillvWvla l l l s l P l l f s w v k t v e e g n g t l n v n v t v C l i
    ++ + ++ + + + + W ++ + l + + P ++ s ++ + g + + n + + + C +
17724 220 MS-RAMCVQLAGAAWAAPFLAMVPT-VLSRAHLDYCHGGV--INHFFCDN 265
    dfpeestasvstwlrsyvl l stlvqFl l P l l v l v c Y t r I l r t l r . . . .
    + ++s+ l+++ +l l + l + l v l + Y + I + t + + ++
17724 266 EPLLQLSCSDTRLLEFWDFLMALTFVLSSFLVTLISYGYIVTTVLripsa 315
    ... kaaktllvvvvvFv l C W l P y f i v l l l d t l c . l s i i m s s t C e l e r v l p
    ++ + a + ++ +++ v + + + l + l + + + + s ++
17724 316 sscQKAFSTCGSHLTLVFIGYSSTIFLYVRPGKaHS-----VQ 353
    t a l l v t l w L a y v N s c l N P i I Y < - *
    + v + l + + + + l N P + I
17724 354 VRKVVALVTSVLTPFLNPFIL 374

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FIG. 3.

FIG. 3



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17724 CV II

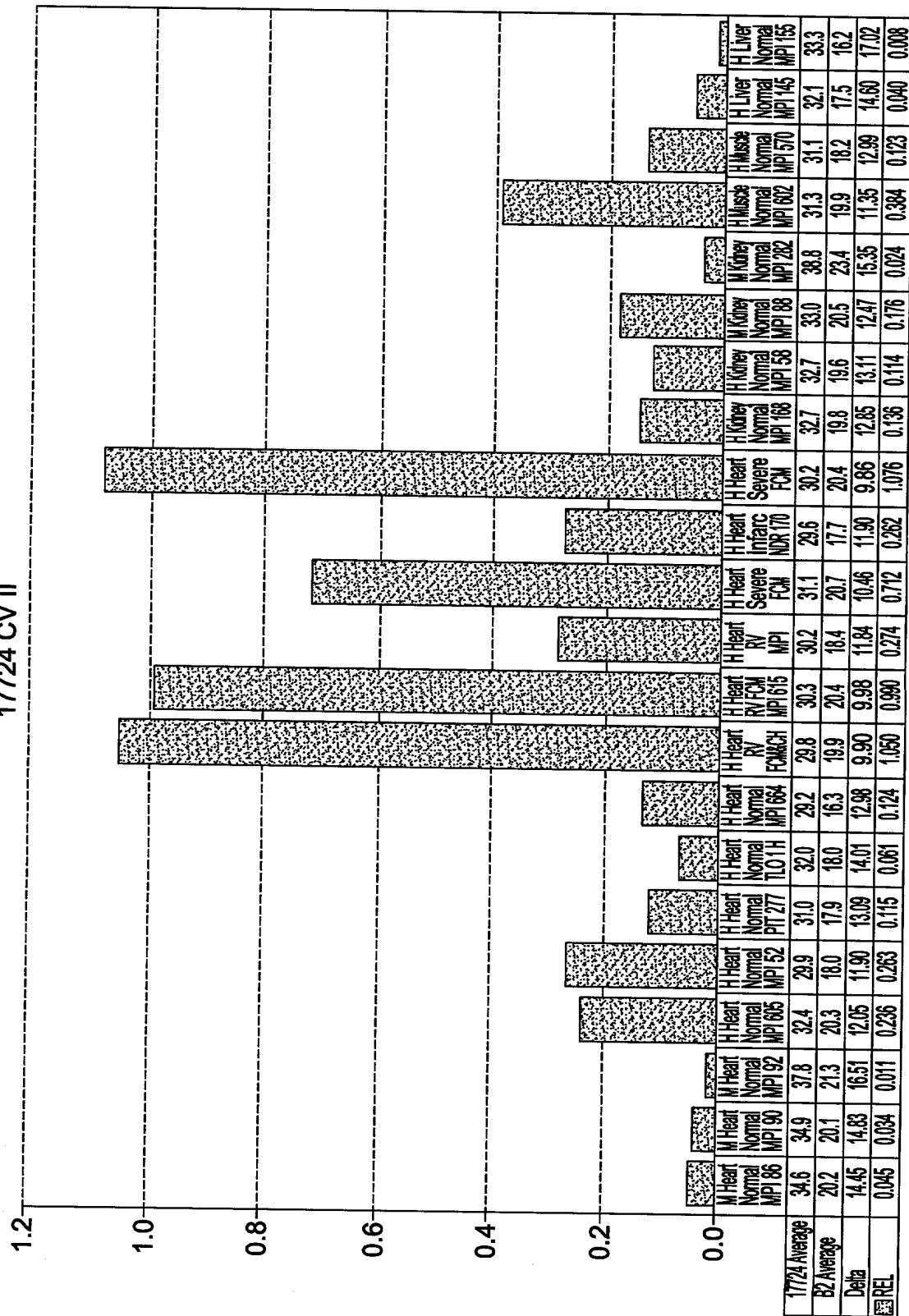
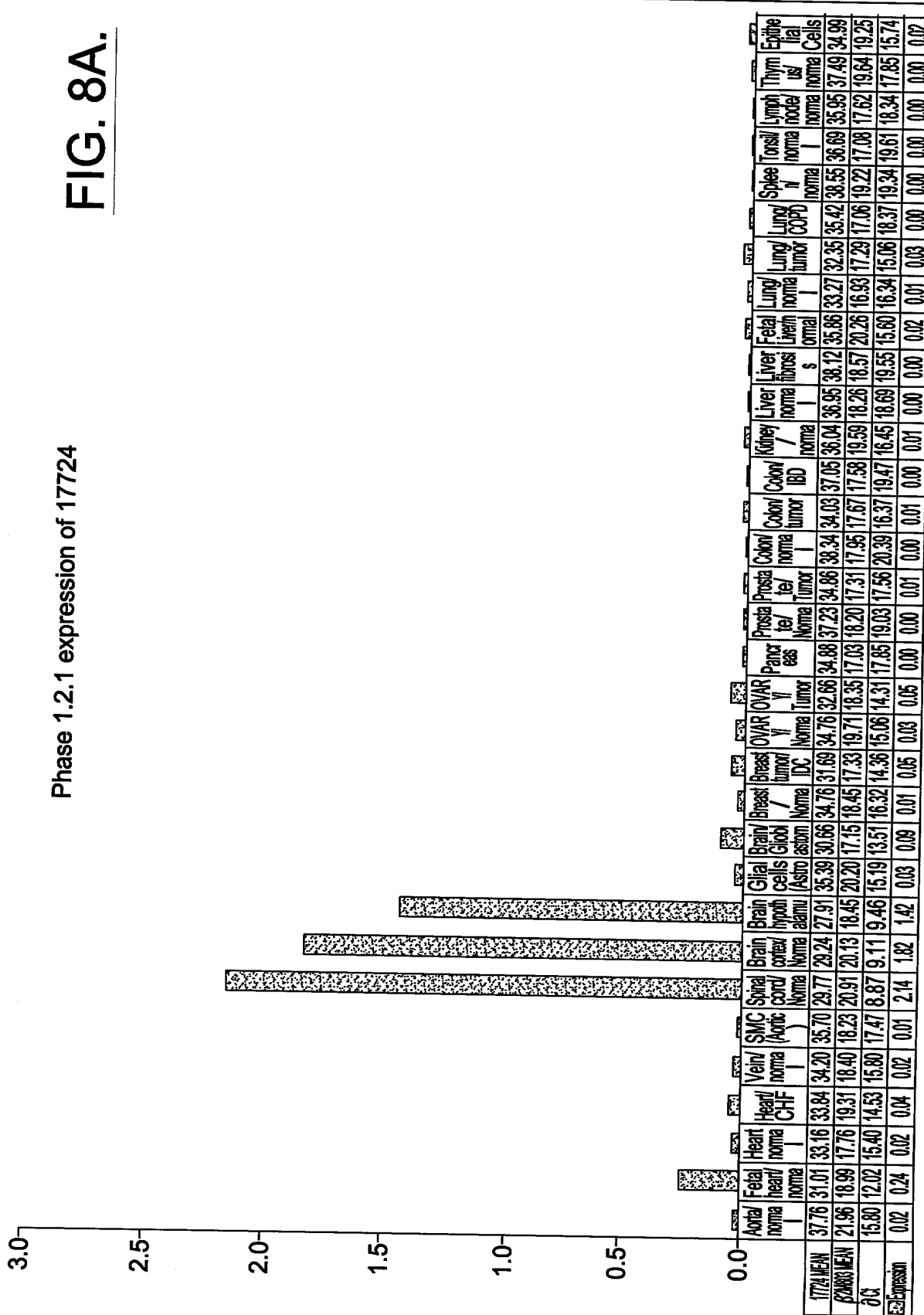


FIG. 6.





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FROM FIG. 8A.

Endo- thelial Cells	Skel- etal Muscl	Fibro- blast (Derm)	Skin/ adipose norma I	Adipo- cyte norma I	Osteo- blast (norma)	Osteo- blast (Diff)	Osteo- blast (static)	Aorta/ SMC (Late)	Aorta/ SMC (Early)	HUVE C	HME C
40.00	32.51	39.05	35.60	35.79	39.16	38.03	37.08	36.40	35.06	37.28	37.58
20.06	18.28	17.75	20.32	17.85	19.67	18.07	17.44	16.75	18.11	20.12	19.74
19.94	14.24	21.30	15.29	17.95	19.50	19.97	19.64	19.66	16.95	17.16	17.84
0.00	0.05	0.00	0.03	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.00

FIG. 8B.

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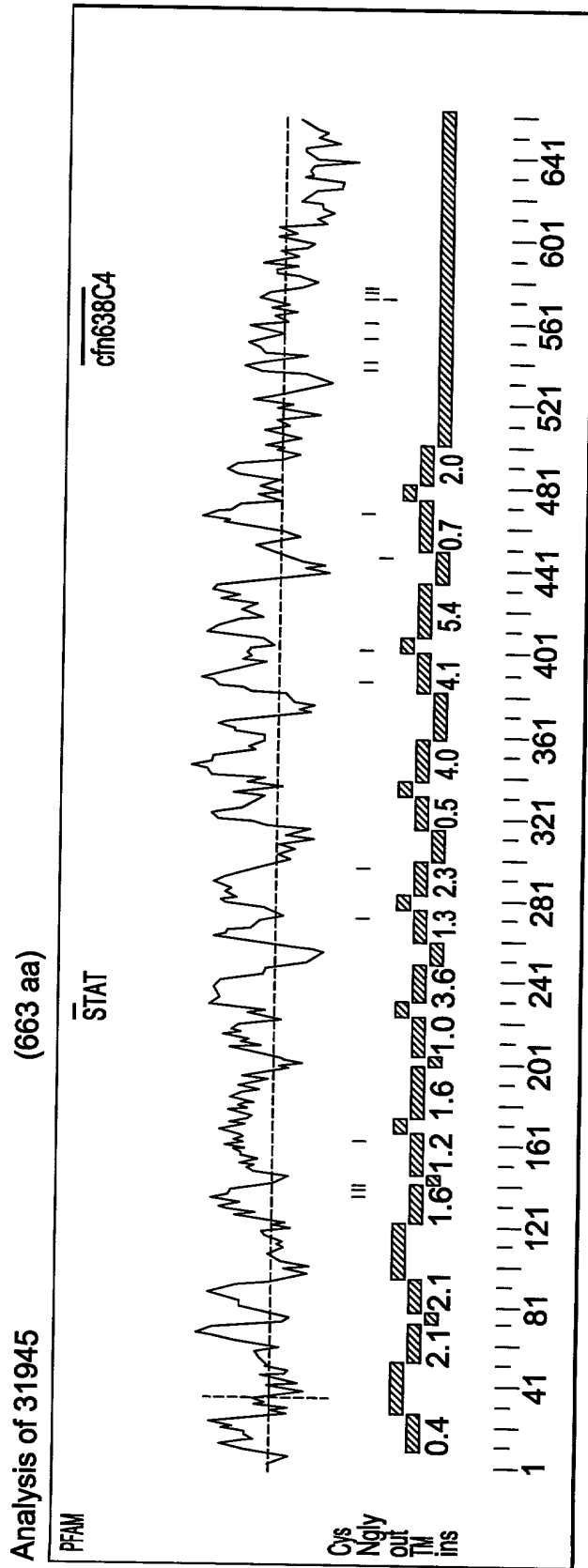


FIG. 9.

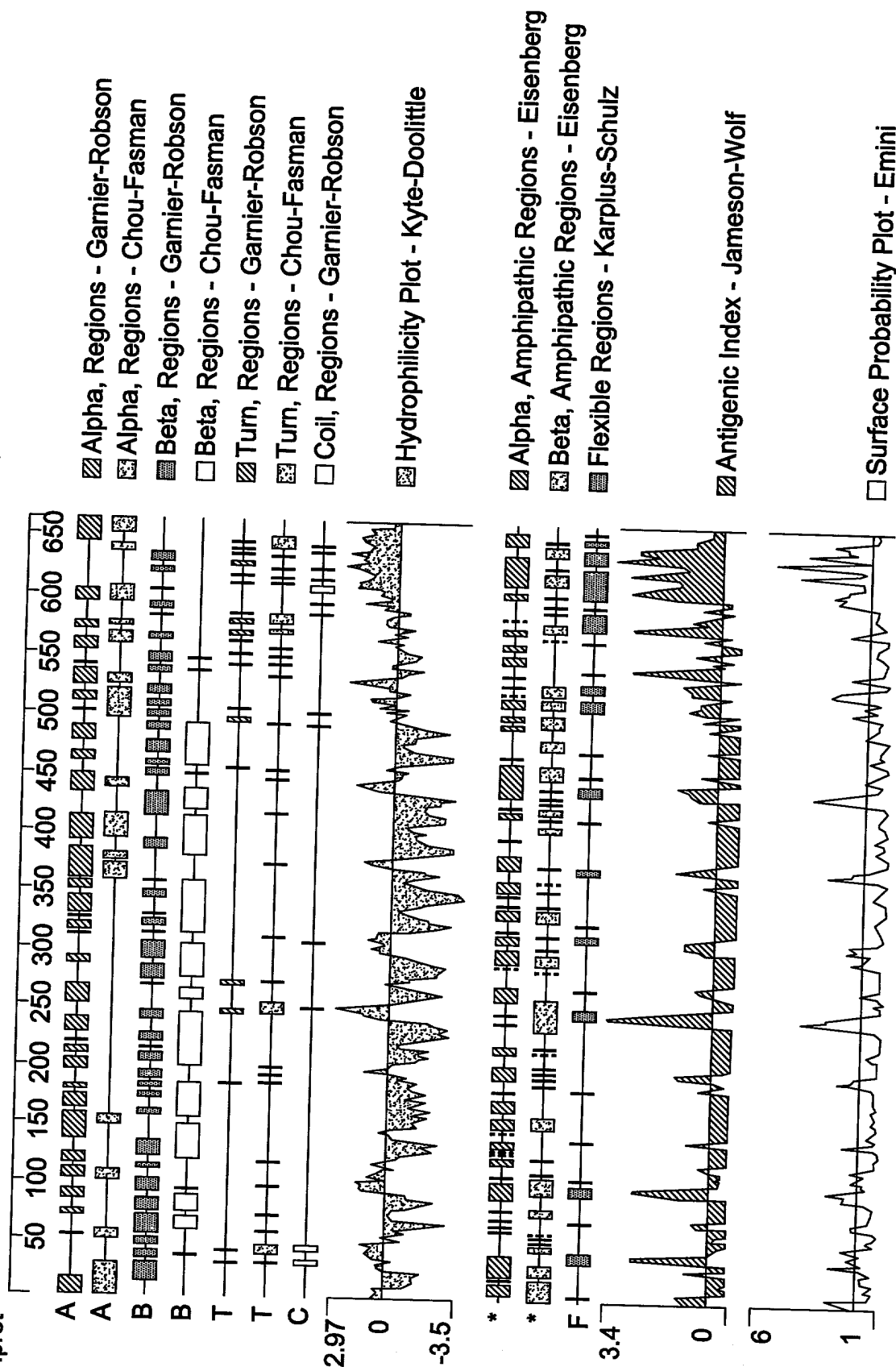


FIG. 10.

TO FIG. 11B.

Taqman Chart+Table GPCR 31945 Expression

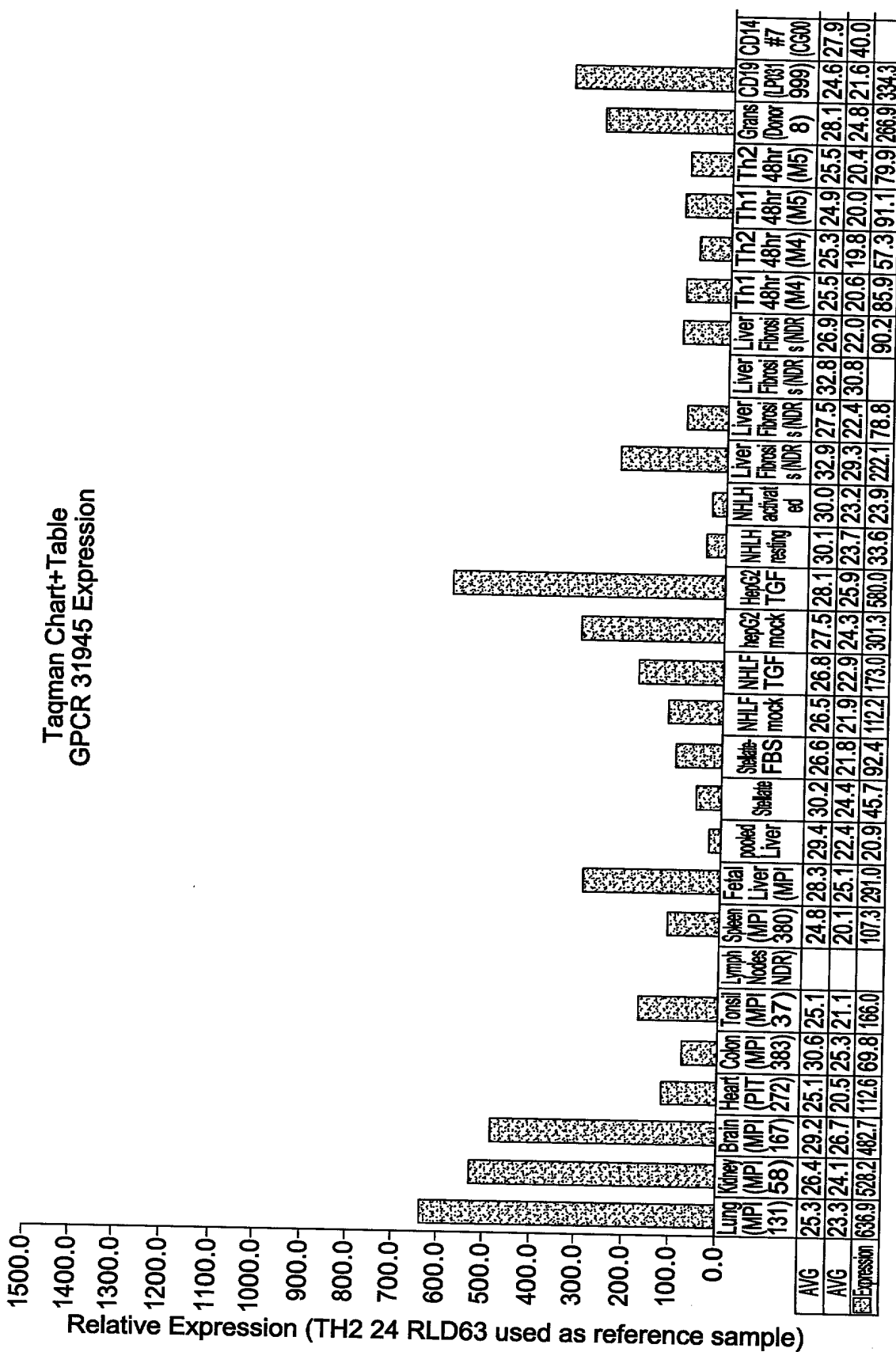


FIG. 11A.

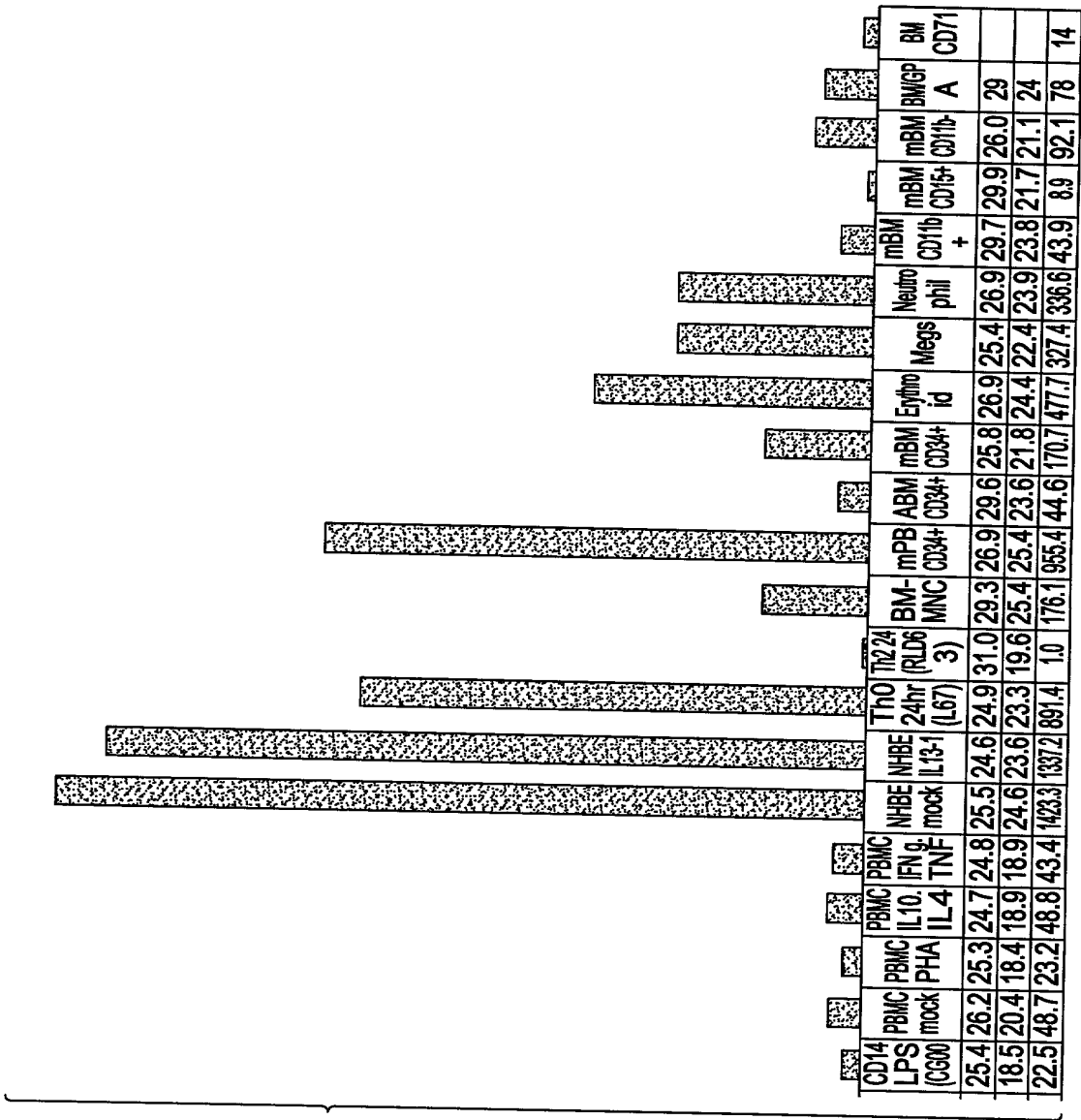


FIG. 11B.

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Analysis of 50288 (372 aa)

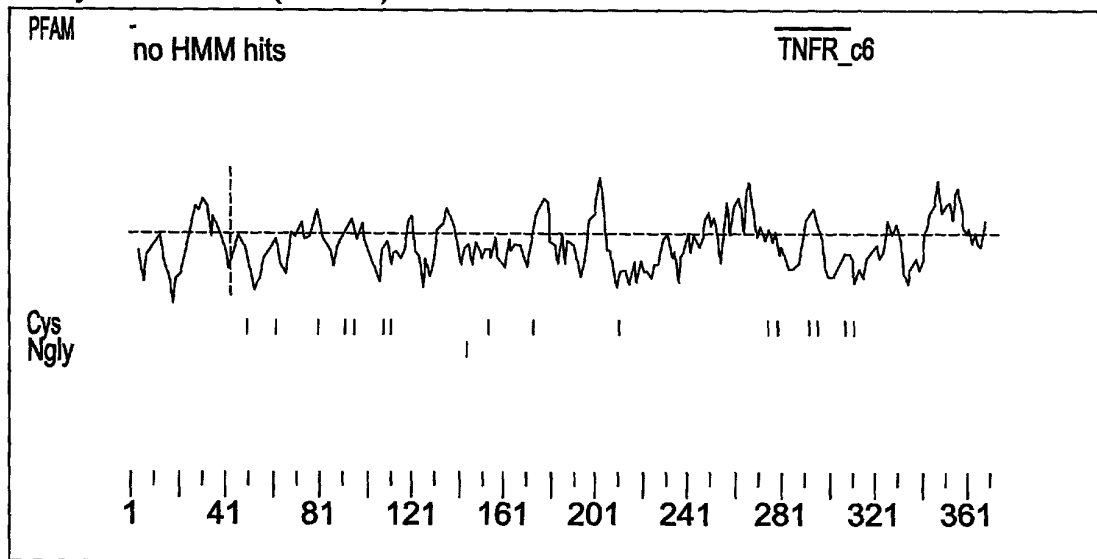


FIG. 12.

09781880 10101

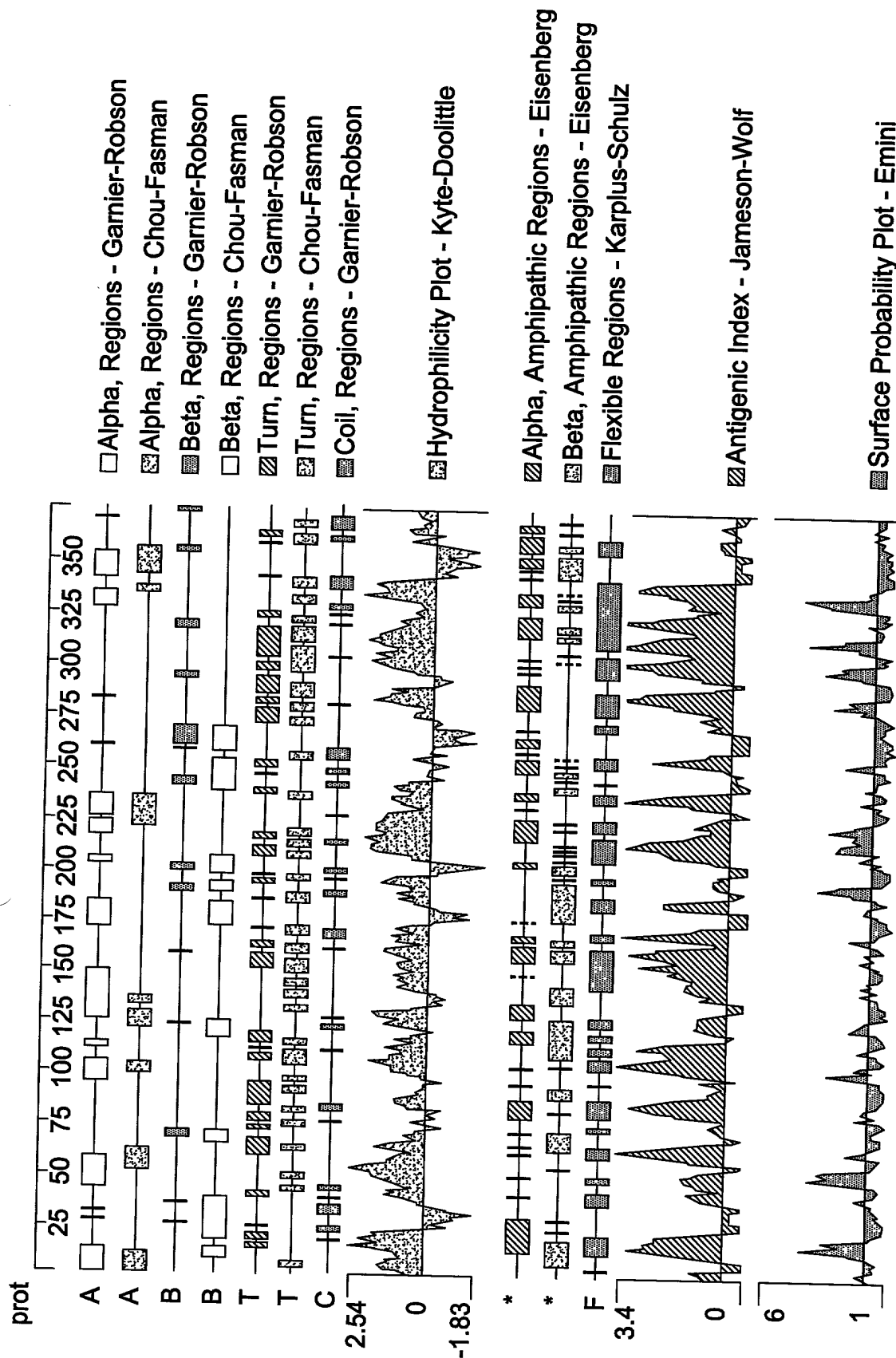


FIG. 13.

Taqman Chart + Table
17724 GPCR Ph 1.9.1 Expression

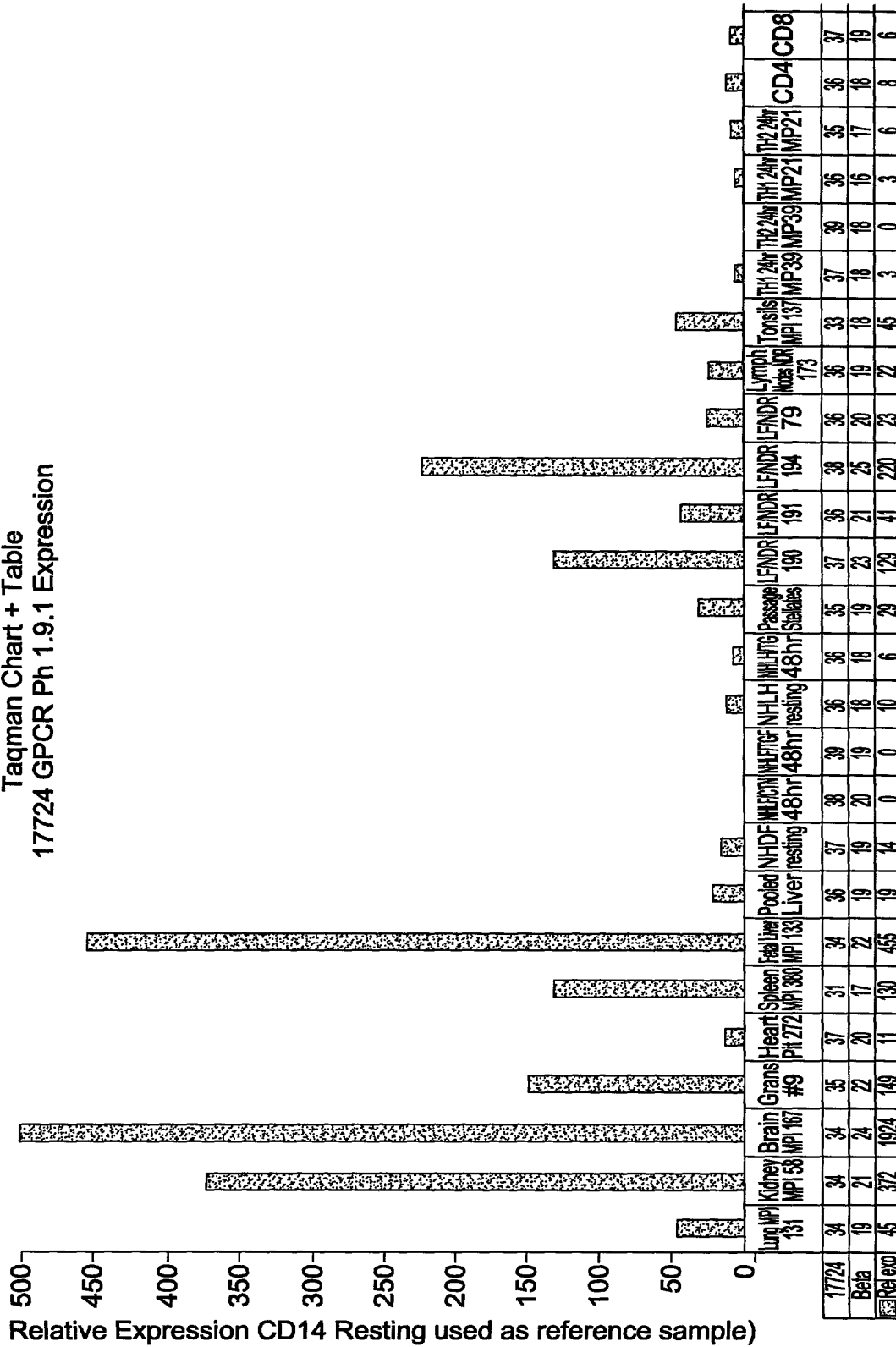
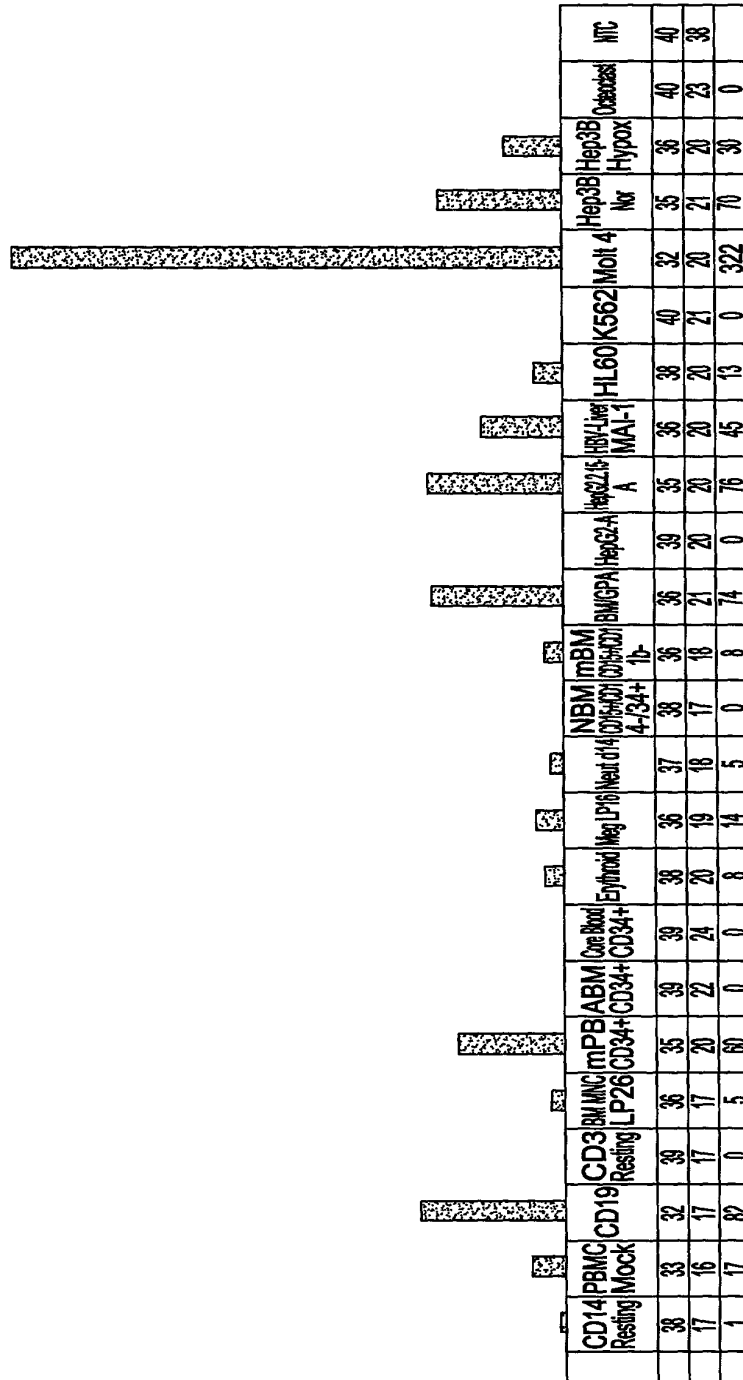


FIG. 14A.

FIG. 14B.



FROM FIG. 14A.

TO FIG. 15B.

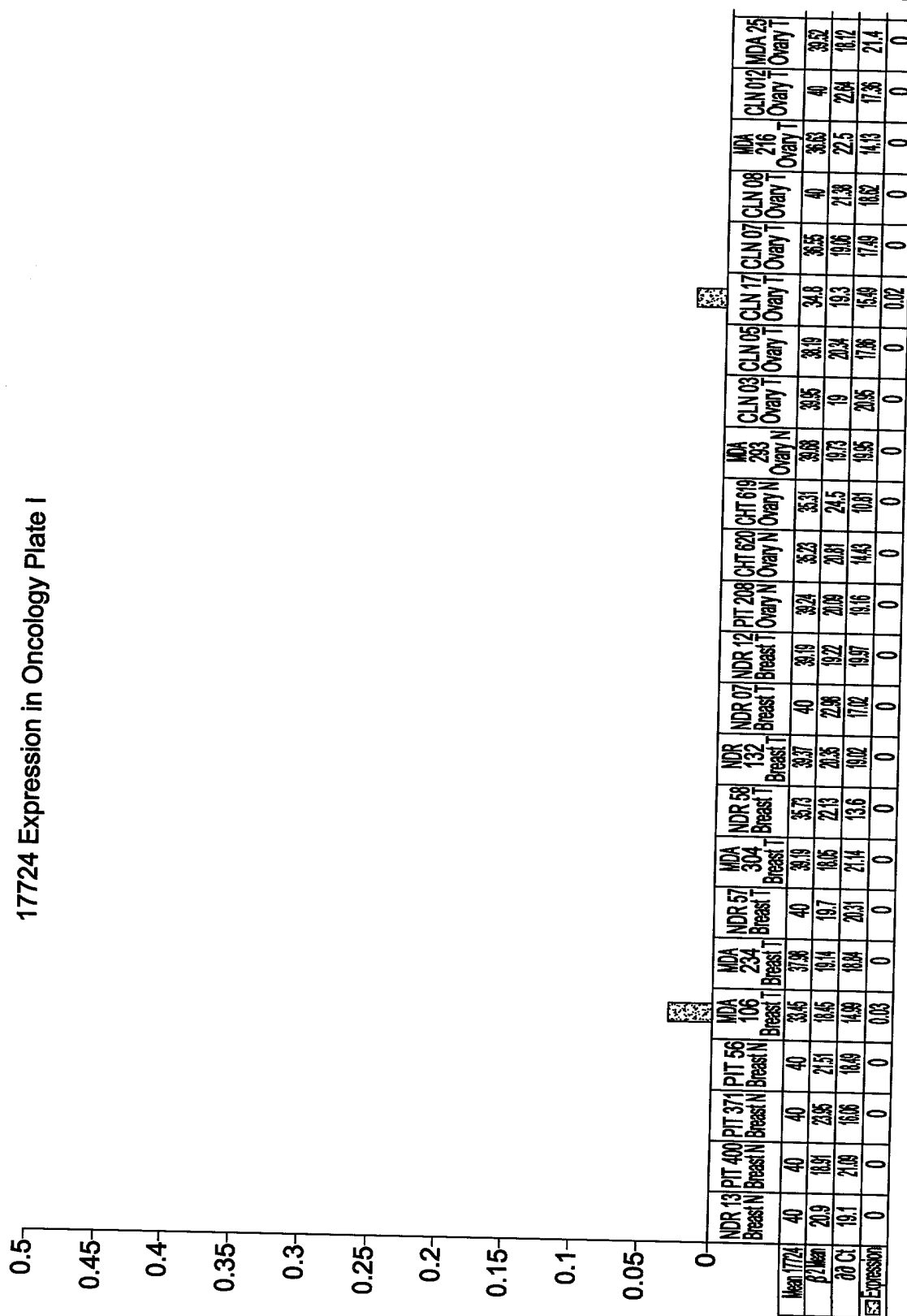
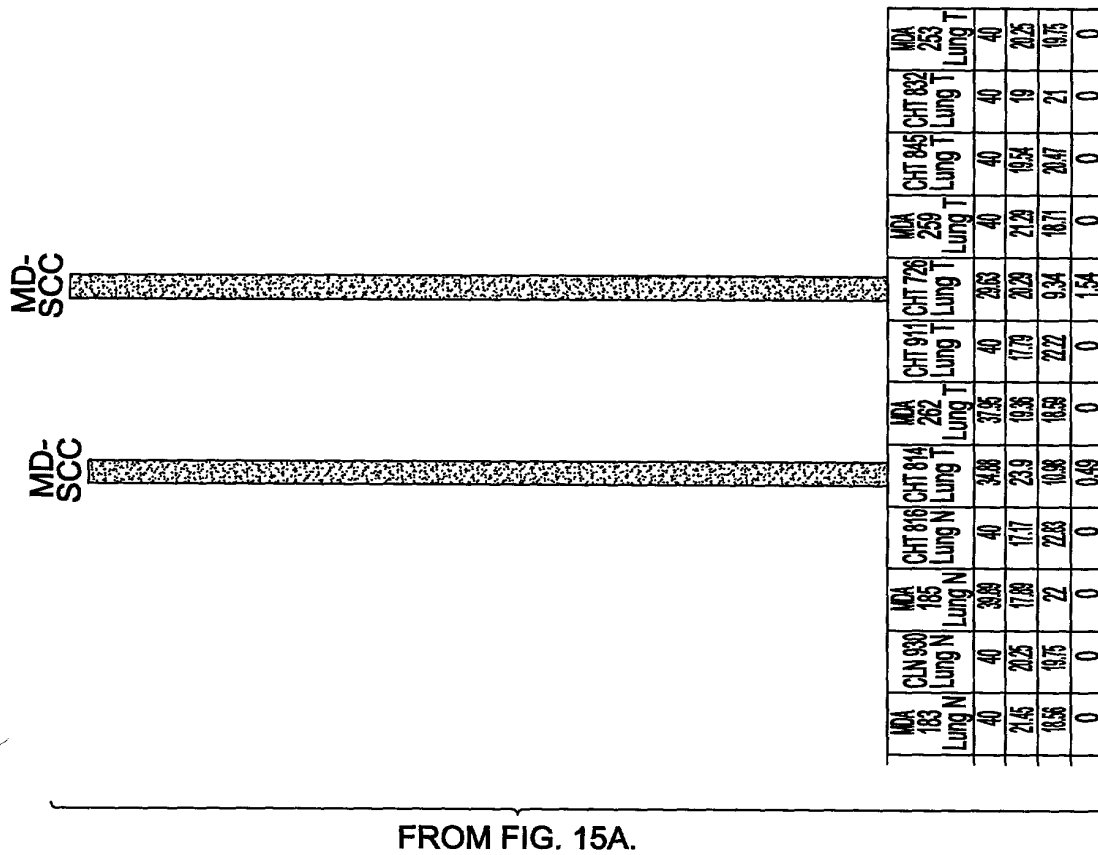


FIG. 15A.



TO FIG. 16B.

FIG. 16A.

17724 CV II and III

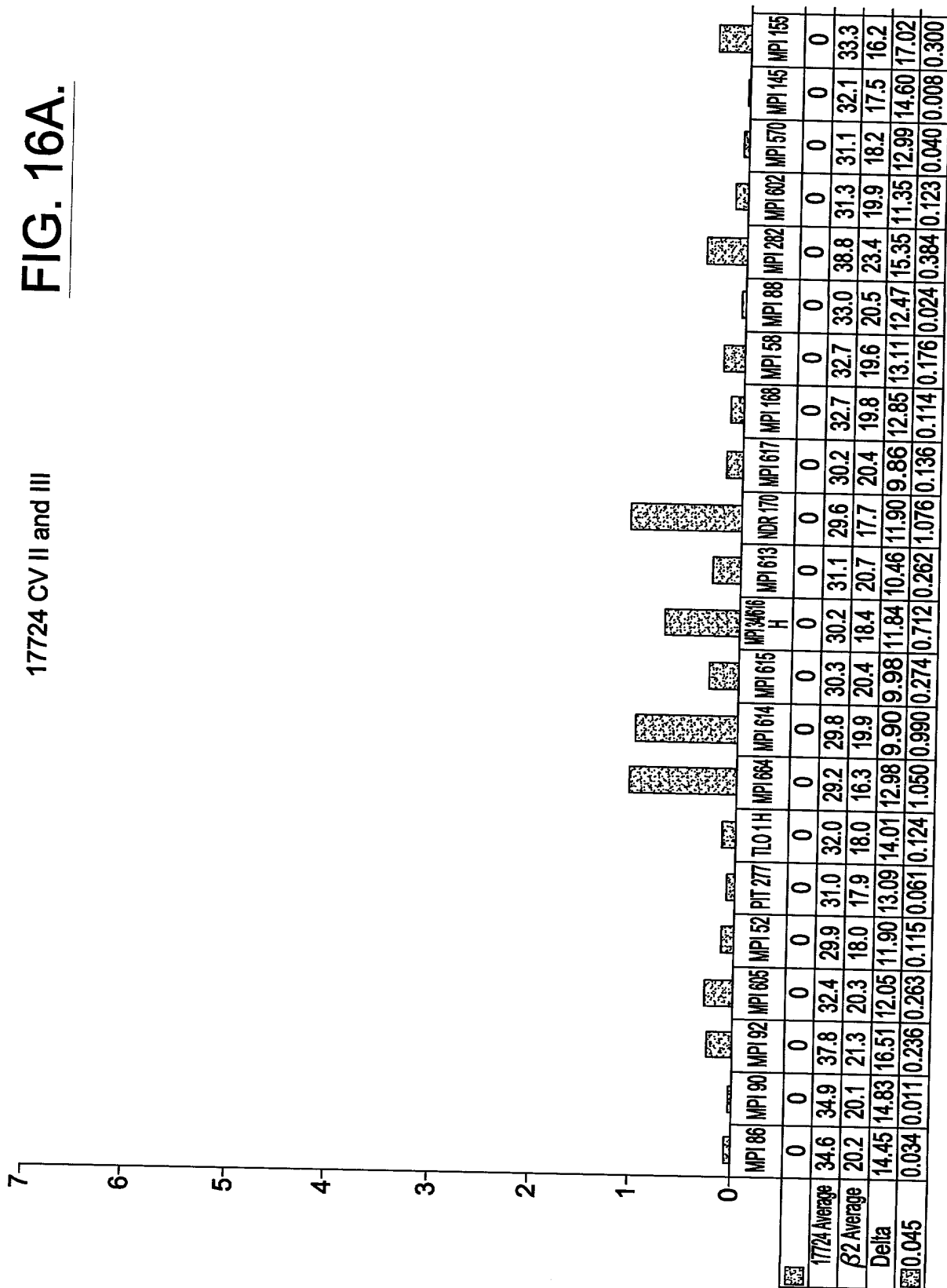
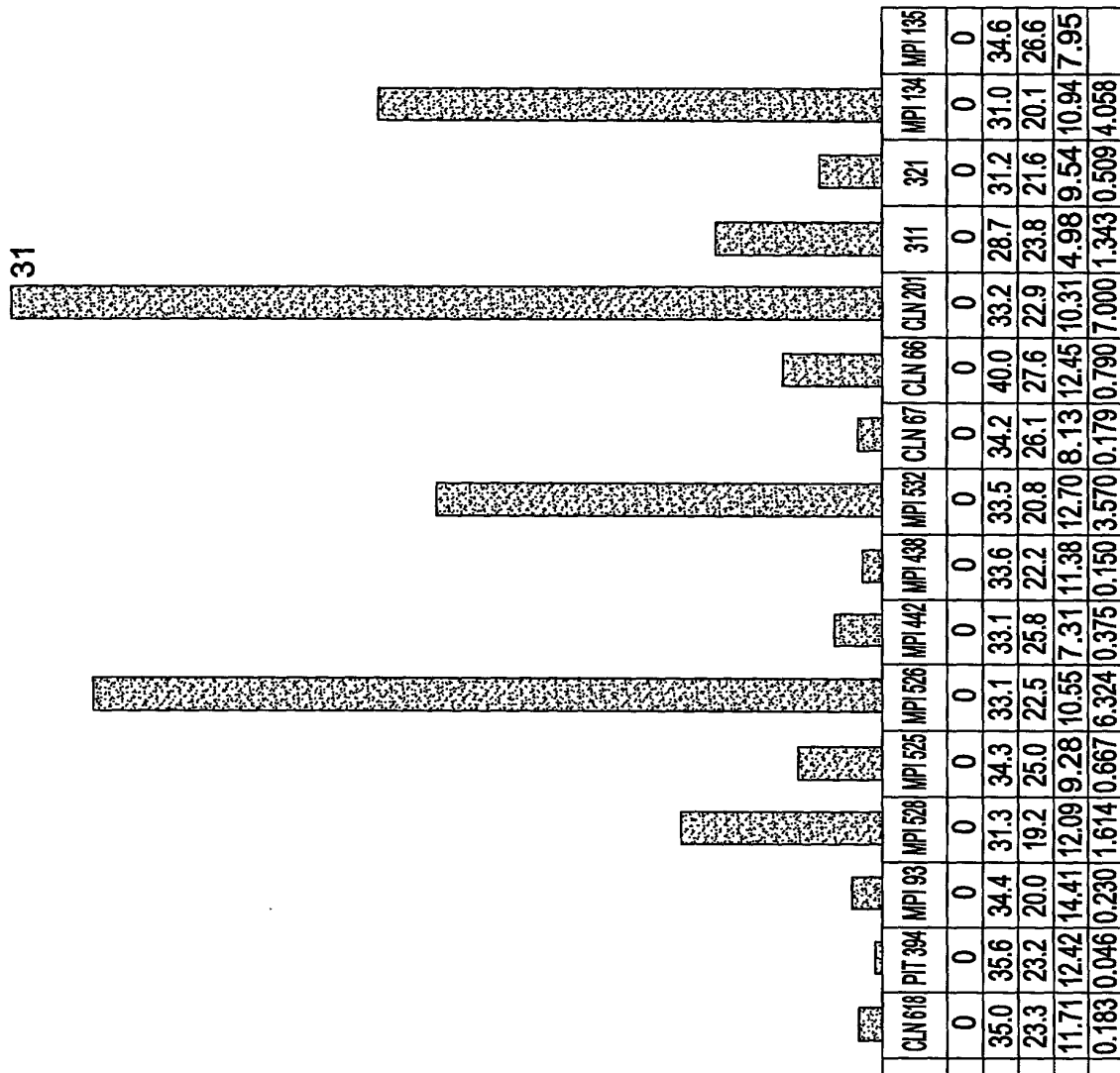


FIG. 16B.



FROM FIG. 16A.

